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RAW SEQUENCE LISTING

DATE: 11/21/2002

PATENT APPLICATION: US/09/899,645A

TIME: 10:13:03

Input Set : A:\5718-111.app

Output Set: N:\CRF4\11212002\I899645A.raw

3 <110> APPLICANT: Li, Chun Ping
 4 Zheng, Peizhong
 5 Nichols, Scott
 7 <120> TITLE OF INVENTION: METHODS FOR REGULATING BETA-OXIDATION IN PLANTS
 9 <130> FILE REFERENCE: 35718/235742
 11 <140> CURRENT APPLICATION NUMBER: 09/899,645A
 12 <141> CURRENT FILING DATE: 2001-07-05
 14 <150> PRIOR APPLICATION NUMBER: 60/216,211
 15 <151> PRIOR FILING DATE: 2000-07-06
 17 <160> NUMBER OF SEQ ID NOS: 8
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1169
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Zea mays
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (89)..(814)
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 33 ggcacgagag actgttgatt gtctaaaa atg gtg cat agt ttg cat gca att 112
 34 Met Val His Ser Leu His Ala Ile
 35 1 5
 37 ttt ctt gtt gct gga gac aat aac ata ccg ata ata tat caa gtt cat 160
 38 Phe Leu Val Ala Gly Asp Asn Asn Ile Pro Ile Ile Tyr Gln Val His
 39 10 15 20
 41 cgg gca cgt gat gga tcc agc ttt gcc aca aga aaa gtg gag gca aag 208
 42 Arg Ala Arg Asp Gly Ser Ser Phe Ala Thr Arg Lys Val Glu Ala Lys
 43 25 30 35 40
 45 cag aag ggc cta gtt gta ttc acc ttg att gct tct ttc cag aag gaa 256
 46 Gln Lys Gly Leu Val Val Phe Thr Leu Ile Ala Ser Phe Gln Lys Glu
 47 45 50 55
 49 gaa gtg ggt ttt gag cat cag gct gca atc atg cct gat gtt cct ccg 304
 50 Glu Val Gly Phe Glu His Gln Ala Ala Ile Met Pro Asp Val Pro Pro
 51 60 65 70
 53 cca gaa cag ctc ctt aat ctg gag gag ata cgt gaa aga cgg ctt act 352
 54 Pro Glu Gln Leu Leu Asn Leu Glu Glu Ile Arg Glu Arg Arg Leu Thr
 55 75 80 85
 57 gat cca cgc ttc cca tcc caa tat agg aac ttg gca gct aaa aaa aag 400
 58 Asp Pro Arg Phe Pro Ser Gln Tyr Arg Asn Leu Ala Ala Lys Lys Lys
 59 90 95 100
 61 ttt att cct tgg ccc ata gaa atg aga ttt tgt gaa ggt tca gcg tct 448
 62 Phe Ile Pro Trp Pro Ile Glu Met Arg Phe Cys Glu Gly Ser Ala Ser

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63 105          110          115          120
65 caa cat aaa cca agc tta aac tac tgg ttt aga gct cga ggg aaa ctc 496
66 Gln His Lys Pro Ser Leu Asn Tyr Trp Phe Arg Ala Arg Gly Lys Leu
67          125          130          135
69 tca gac gac caa gct cta cac aga tgt gtt gta gca tat gct tcg gat 544
70 Ser Asp Asp Gln Ala Leu His Arg Cys Val Val Ala Tyr Ala Ser Asp
71          140          145          150
73 cta cta ttt tct ggg gtg agc ctt aac cct cat cgg gag aag ggt ttg 592
74 Leu Leu Phe Ser Gly Val Ser Leu Asn Pro His Arg Glu Lys Gly Leu
75          155          160          165
77 aag aca tac tgc ctc agt ctt gac cat tcc atc tgg ttc cac aaa cct 640
78 Lys Thr Tyr Cys Leu Ser Leu Asp His Ser Ile Trp Phe His Lys Pro
79          170          175          180
81 gtg aag gct gac gaa tgg atg ctg tat gtg atc gag agc cca tct gcg 688
82 Val Lys Ala Asp Glu Trp Met Leu Tyr Val Ile Glu Ser Pro Ser Ala
83 185          190          195          200
85 cac ggt ggt cgc ggt ttc gtc acc gga cgc atg ttc aac agg caa gga 736
86 His Gly Gly Arg Gly Phe Val Thr Gly Arg Met Phe Asn Arg Gln Gly
87          205          210          215
89 gag ctt atc atg tcg ctg acc caa gag gca ttg att cga agg gag aag 784
90 Glu Leu Ile Met Ser Leu Thr Gln Glu Ala Leu Ile Arg Arg Glu Lys
91          220          225          230
93 ccg cga gga cca aat ccg agg ccg aag ctt tgaggcacct gacagcctct 834
94 Pro Arg Gly Pro Asn Pro Arg Pro Lys Leu
95          235          240
97 gcagtcgact gtagaggatc ccaaccgagc tttgagaggc gcaccatcct ttctttcta 894
99 ttggtttaga tatttatgaa ttcacaaaca aaaatataga atatcaagca gtataaaaga 954
101 tctcaagtca aacctaacat tttttttcat ttctccggat gattttctatt tgttttggtg 1014
103 tgtgtgtggt tggaggggta ttggaagcgg aagcggaggc ggaggggttg atactttagg 1074
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113 <213> ORGANISM: Zea mays
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119 Ile Pro Ile Ile Tyr Gln Val His Arg Ala Arg Asp Gly Ser Ser Phe
120 20 25 30
122 Ala Thr Arg Lys Val Glu Ala Lys Gln Lys Gly Leu Val Val Phe Thr
123 35 40 45
125 Leu Ile Ala Ser Phe Gln Lys Glu Glu Val Gly Phe Glu His Gln Ala
126 50 55 60
128 Ala Ile Met Pro Asp Val Pro Pro Glu Gln Leu Leu Asn Leu Glu
129 65 70 75 80
131 Glu Ile Arg Glu Arg Arg Leu Thr Asp Pro Arg Phe Pro Ser Gln Tyr
132 85 90 95
134 Arg Asn Leu Ala Ala Lys Lys Lys Phe Ile Pro Trp Pro Ile Glu Met

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135		100		105		110	
137	Arg	Phe	Cys	Glu	Gly	Ser	Ala
138			115			120	
140	Trp	Phe	Arg	Ala	Arg	Gly	Lys
141		130				135	
143	Cys	Val	Val	Ala	Tyr	Ala	Ser
144	145				150		155
146	Asn	Pro	His	Arg	Glu	Lys	Gly
147				165			170
149	His	Ser	Ile	Trp	Phe	His	Lys
150			180				185
152	Tyr	Val	Ile	Glu	Ser	Pro	Ser
153			195				200
155	Gly	Arg	Met	Phe	Asn	Arg	Gln
156		210				215	
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181	Gly	Asp	Pro	Pro	Gly	Asp	Leu
182			20			25	
184	aac	ctc	gag	ccg	ctg	gac	gag
185	Asn	Leu	Glu	Pro	Leu	Asp	Glu
186		35				40	
188	gta	ccg	gcc	aag	agg	ctg	ttt
189	Val	Pro	Ala	Lys	Arg	Leu	Phe
190		50				55	
192	gtg	gct	gca	gcc	aag	tct	gtg
193	Val	Ala	Ala	Ala	Lys	Ser	Val
194	65				70		75
196	cac	tgc	tac	ttt	gtt	cgg	gca
197	His	Cys	Tyr	Phe	Val	Arg	Ala
198				85			90
200	caa	gtg	gag	cgg	aca	cga	aca
201	Gln	Val	Glu	Arg	Thr	Arg	Thr
202			100				105
204	aag	gcc	gtg	caa	cat	ggg	aag
205	Lys	Ala	Val	Gln	His	Gly	Lys

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209 Gln Gln Ala Gln Pro Ser Pro Met Gln His Gln Phe Ser Met Pro Thr
210          130          135          140
212 gtg cca cca cca gaa gag ctg ctt gac tgt gag acc ctc att gac cag 480
213 Val Pro Pro Pro Glu Glu Leu Leu Asp Cys Glu Thr Leu Ile Asp Gln
214 145          150          155          160
216 tat tta agg gac cct aac ctc caa aag agg tac cca ttg gcg ctc aac 528
217 Tyr Leu Arg Asp Pro Asn Leu Gln Lys Arg Tyr Pro Leu Ala Leu Asn
218          165          170          175
220 cga att gct gct cag gag gtc ccc att gag atc aag cca gta aac cca 576
221 Arg Ile Ala Ala Gln Glu Val Pro Ile Glu Ile Lys Pro Val Asn Pro
222          180          185          190
224 tcc ccc ctg agc cag ctg cag aga atg gag ccc aaa cag atg ttc tgg 624
225 Ser Pro Leu Ser Gln Leu Gln Arg Met Glu Pro Lys Gln Met Phe Trp
226          195          200          205
228 gtg cga gcc cgg ggc tat att ggc gag ggc gac atg aag atg cac tgc 672
229 Val Arg Ala Arg Gly Tyr Ile Gly Glu Gly Asp Met Lys Met His Cys
230          210          215          220
232 tgc gtg gcc gcc tat atc tcc gac tat gcc ttc ttg ggc act gca ctg 720
233 Cys Val Ala Ala Tyr Ile Ser Asp Tyr Ala Phe Leu Gly Thr Ala Leu
234 225          230          235          240
236 ctg cct cac cag tgg cag cac aag gtg cac ttc atg gtc tca ctg gac 768
237 Leu Pro His Gln Trp Gln His Lys Val His Phe Met Val Ser Leu Asp
238          245          250          255
240 cat tcc atg tgg ttc cac gcc ccc ttc cga gct gac cac tgg atg ctc 816
241 His Ser Met Trp Phe His Ala Pro Phe Arg Ala Asp His Trp Met Leu
242          260          265          270
244 tat gaa tgc gag agc ccc tgg gcc ggt ggc tct cgg ggg ctg gtc cat 864
245 Tyr Glu Cys Glu Ser Pro Trp Ala Gly Gly Ser Arg Gly Leu Val His
246          275          280          285
248 ggg cgg ctg tgg cgt cag gat gga gtc cta gct gtg acc tgt gcc cag 912
249 Gly Arg Leu Trp Arg Gln Asp Gly Val Leu Ala Val Thr Cys Ala Gln
250          290          295          300
252 gag ggc gtg atc cga gtg aag ccc cag gtc tca gag agc aag ctg tag 960
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254 305          310          315
257 <210> SEQ ID NO: 4
258 <211> LENGTH: 319
259 <212> TYPE: PRT
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264 1          5          10          15
266 Gly Asp Pro Pro Gly Asp Leu Arg Ser Val Leu Val Thr Thr Val Leu
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269 Asn Leu Glu Pro Leu Asp Glu Asp Leu Phe Arg Gly Arg His Tyr Trp
270          35          40          45
272 Val Pro Ala Lys Arg Leu Phe Gly Gly Gln Ile Val Gly Gln Ala Leu

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273      50      55      60
275 Val Ala Ala Ala Lys Ser Val Ser Glu Asp Val His Val His Ser Leu
276 65      70      75      80
278 His Cys Tyr Phe Val Arg Ala Gly Asp Pro Lys Leu Pro Val Leu Tyr
279      85      90      95
281 Gln Val Glu Arg Thr Arg Thr Gly Ser Ser Phe Ser Val Arg Ser Val
282      100      105      110
284 Lys Ala Val Gln His Gly Lys Pro Ile Phe Ile Cys Gln Ala Ser Phe
285      115      120      125
287 Gln Gln Ala Gln Pro Ser Pro Met Gln His Gln Phe Ser Met Pro Thr
288      130      135      140
290 Val Pro Pro Pro Glu Glu Leu Leu Asp Cys Glu Thr Leu Ile Asp Gln
291 145      150      155      160
293 Tyr Leu Arg Asp Pro Asn Leu Gln Lys Arg Tyr Pro Leu Ala Leu Asn
294      165      170      175
296 Arg Ile Ala Ala Gln Glu Val Pro Ile Glu Ile Lys Pro Val Asn Pro
297      180      185      190
299 Ser Pro Leu Ser Gln Leu Gln Arg Met Glu Pro Lys Gln Met Phe Trp
300      195      200      205
302 Val Arg Ala Arg Gly Tyr Ile Gly Glu Gly Asp Met Lys Met His Cys
303      210      215      220
305 Cys Val Ala Ala Tyr Ile Ser Asp Tyr Ala Phe Leu Gly Thr Ala Leu
306 225      230      235      240
308 Leu Pro His Gln Trp Gln His Lys Val His Phe Met Val Ser Leu Asp
309      245      250      255
311 His Ser Met Trp Phe His Ala Pro Phe Arg Ala Asp His Trp Met Leu
312      260      265      270
314 Tyr Glu Cys Glu Ser Pro Trp Ala Gly Gly Ser Arg Gly Leu Val His
315      275      280      285
317 Gly Arg Leu Trp Arg Gln Asp Gly Val Leu Ala Val Thr Cys Ala Gln
318      290      295      300
320 Glu Gly Val Ile Arg Val Lys Pro Gln Val Ser Glu Ser Lys Leu
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325 <210> SEQ ID NO: 5

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327 <212> TYPE: DNA

328 <213> ORGANISM: *Saccharomyces cerevisiae*

330 <220> FEATURE:

331 <221> NAME/KEY: CDS

332 <222> LOCATION: (501)..(1547)

334 <400> SEQUENCE: 5

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339 acaatagcga agacaatgat gacgctagcc atcggtctgaa gcgtgcggcc aggaccatta 180
341 ttccctggga ggaactaaga cccgacactc tggaatctga gctgtgaaac gggcgctctg 240
343 ctttttcatt ctacacaggc atatgtaaca gcagtgtata ggctatgtaa atcggcccaa 300
345 tcaacaacaa agcgttgctt attggacttg ctactacccc aacaaaggag agagcctttg 360
347 attgcatacct cggaagagac ggcataaaca ccgagcctca tcctacaatg aaaaaccacg 420
349 ccagttggat ataaaccaga aaagggtttc aattcagtat ccacatgag caagacaaga 480

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VERIFICATION SUMMARY

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